WHAT IS CLAIMED IS:

1. A method of identifying agents that kill or arrest growth in a cell, comprising:
   (a) introducing an initial library of putative negative selection agents into a cell population;
   (b) propagating the cell population;
   (c) re-isolating the library components from the propagated cell population; and
   (d) subjecting the initial and re-isolated library components to quantitative comparison of the relative amounts of at least one specific library component.

2. The method of claim 1, further comprising as enrichment step (e), in which the library components from step (c) are subjected to one or more cycles of steps (a) through (c).

3. The method of claim 1, wherein the library of putative negative selection agents is a genetic library.

4. The method of claim 3, wherein the library comprises inserts selected from the group consisting of genomic DNA, cDNA and random sequence DNA.

5. The method of claim 3, wherein the genetic library comprises a plurality of inserts, the inserts comprising one or more sequences which, upon expression in a living cell, are capable of differentially altering the phenotype of the host

cell.

6. The method of claim 5, wherein expression of the sequences alters host cell gene expression.

7. The method of claim 1, wherein step (d) further comprises:
(d1) differentially labeling nucleic acid samples derived from the initial and propagated libraries to generate a first and second labeled nucleic acid sample;
(d2) generating a target pool comprising said first and second nucleic acid samples,
(d3) contacting said target pool with a plurality of solid supports each having attached thereto multiple capture oligonucleotides of a unique sequence under conditions which promote the formation of perfectly matched duplexes between said capture oligonucleotides and nucleic acid molecule components within said target pool; and
(d4) sorting the solid supports according to the relative amount of said first label and said second label.

8. The method of claim 7, wherein the unique capture oligonucleotides attached to the solid supports have a length of from about 10 to about 100 nucleotides.

9. The method of claim 7, wherein the unique capture oligonucleotides attached to the solid supports comprise a combination of from about 2 to about 6 sequence units in tandem configuration, each unit consisting of from about 7 to about 15 nucleotides.

10. The method of claim 7, wherein the target nucleic acid molecules have

attached thereto unique oligonucleotide identifier tags, each of said tags comprising a combination of from about 2 to about 6 sequence units in tandem configuration, each unit consisting of from about 7 to about 15 nucleotides.

11. The method of claim 10, wherein the capture oligonucleotides attached to said solid supports comprise complements of said unique identifier tags.

12. The method of claim 7, wherein said first and said second label are distinguishable fluorescent labels.

13. The method of claim 12, wherein said fluorescent labels are individually selected from the group consisting of 6FAM, HEX, TET, TAMRA, ROX, JOE, 5-FAM, phycoerythrin and R110.

14. The method of claim 12, wherein one of said fluorescent labels is FITC.

15. The method of claim 1, wherein the cell populations in step (a) differ in phenotype.

16. The method of claim 1, wherein the cell populations in step (a) differ in genotype.

17. The method of claim 1, wherein the cell populations in step (a) comprise cells which differ in cell type, tissue type, physiological state, disease state or developmental stage.

18. The method of claim 1, wherein the cell populations in step (a) comprise

cancerous and non-cancerous cells, respectively.

19. The method of claim 1, wherein the cell populations in step (a) comprise cells before and after treatment with an agent, respectively.

20. The method of claim 19, wherein the agent is selected from the group consisting of a naturally occurring growth factor, an immunologic factor, a small molecule compound of interest, a putative therapeutic compound, a therapeutic lead compound, and a growth-arresting substance.

21. A method of identifying a negative selection agent that causes a member of a cell population to be lost from that population, comprising:

(a) providing a cell population with a tagged pre-passage library, each member of said library comprising a sequence identifier tag and DNA encoding a corresponding putative negative selection agent;

(b) passaging said cell population to generate a post-passage cell subpopulation;

(c) isolating from said post-passage cell subpopulation a corresponding tagged post-passage sublibrary;

(d) comparing sequence identifier tags in said pre-passage library to sequence identifier tags in said post-passage sublibrary to identify an sequence identifier tag of a lost library member; and

(e) identifying a negative selection agent that corresponds with said lost library member sequence identifier tag.

22. The method of claim 21 wherein said sequence identifier tag comprises a combination of from about 2 to about 6 sequence units in tandem

configuration, each unit consisting of from about 7 to about 15 nucleotides.

23. The method of claim 22 wherein said combination consists of 3 sequence units, each unit consisting of 8 nucleotides.

24. The method of claim 21, wherein step (d) further comprises:

(d1) for each member of said post-passage sublibrary, separating said sequence identifier tag from said corresponding putative negative selection agent;

(e2) segregating each said separated sequence identifier tag; and

(e3) using each said segregated sequence identifier tag to segregate a corresponding negative selection agent from said sublibrary.

25. The method of claim 24, wherein said step of segregating comprises adhering a fluorochrome to said separated tag to form a fluorescent complex, and isolating said fluorescent complex.

26. The method of claim 25, wherein said step of isolating each said fluorescent complex is performed with a fluorescence-activated sorter.

27. The method of claim 25, wherein said fluorochrome is FITC.

28. The method of claim 25, wherein said fluorochrome is attached to a solid support.

29. The method of claim 24, wherein each said segregated tag is a primer for amplifying each said corresponding negative selection agent.

30. A method of identifying selective lethality agent that kills members of a first cell

population but not of a second cell population, comprising:

(f) providing both a first cell population and a second cell population with a tagged pre-passage library, each member of said library comprising DNA encoding an sequence identifier tag and a putative selective lethality agent;

(g) passaging said first and said second cell populations;

(h) collecting a first and a second post-passage cell subpopulation;

(i) isolating from said first and second post-passage cell subpopulations corresponding first and second tagged post-passage sublibraries;

(j) comparing said first pre-passage library to said first post-passage sublibrary to identify a first set of lost library members;

(k) comparing said second pre-passage library to said second post-passage sublibrary to identify a second set of lost library members;

(l) identifying a cell-specific lost library member that is in said first set of lost library members but not in said second set of lost library members; and

(m) correlating said cell-specific lost library member with a corresponding selective lethality agent.

31. The method of claim 21 or 30, wherein step (d) further comprises:

(d1) transcribing said sequence identifier tags in said pre-passage library and in said post-passage sublibrary;

(d2) labeling said pre-passage sequence identifier tags with a first fluorochrome and said post-passage sequence identifier tags with a second fluorochrome;

(d3) hybridizing all fluorochrome-labeled sequence identifier tags with a set of support having attached capture oligonucleotides; and

(d4) isolating a subpopulation of supports that hybridized only to said first fluorocrome.